

**JOINT INVENTORS**

**APPLICATION FOR  
UNITED STATES LETTERS PATENT**

**S P E C I F I C A T I O N**

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**TO ALL WHOM IT MAY CONCERN:**

Be it known that we, **ROBERT E. FERRELL**, a citizen of the United States of America, residing at Pittsburgh, Pennsylvania, and **KARI ALITALO**, a citizen of Finland, residing at Helsinki, FINLAND, and **DAVID N. FINEGOLD**, a citizen of the United States of America, residing at Pittsburgh, Pennsylvania, and **MARIKA KARKKAINEN**, a citizen of Finland, residing at Helsinki, FINLAND have invented a new and useful **SCREENING AND THERAPY FOR LYMPHATIC DISORDERS INVOLVING THE FLT4 RECEPTOR TYROSINE KINASE (VEGFR-3)**, of which the following is a specification.

**SCREENING AND THERAPY FOR  
LYMPHATIC DISORDERS INVOLVING THE  
FLT4 RECEPTOR TYROSINE KINASE (VEGFR-3)**

5 This application is a Continuation-in-Part of International Patent  
Application No. PCT/US99/06133, filed March 26, 1999, incorporated herein by  
reference in its entirety.

**ACKNOWLEDGMENT OF GOVERNMENT SUPPORT**

10 This invention was made with United States and Finnish government  
support, including support under contract R03-HD35174, awarded by the U.S.  
National Institutes of Health. The U.S. Government has certain rights in this  
invention.

**FIELD OF THE INVENTION**

15 The present invention relates generally to the fields of molecular  
biology and medicine; more particularly to the areas of genetic screening and the  
identification and treatment of hereditary disorders; and more particularly to  
identification and treatment of hereditary lymphedema.

**DESCRIPTION OF RELATED ART**

20 The lymphatic system is a complex structure organized in parallel  
fashion to the circulatory system. In contrast to the circulatory system, which utilizes  
the heart to pump blood throughout the body, the lymphatic system pumps lymph fluid  
using the inherent contractility of the lymphatic vessels. The lymphatic vessels are not  
interconnected in the same manner as the blood vessels, but rather form a set of  
coordinated structures including the initial lymphatic sinuses [Jeltsch *et al.*, *Science*,  
276:1423-1425 (1997); and Castenholz, A., in Olszewski, W.L. (ed.), *Lymph Stasis:*  
25 *Pathophysiology, Diagnosis, and Treatment*. CRC Press: Boca Raton, Florida (1991),  
pp.15-42] which drain into the lymphatic capillaries and subsequently to the collecting  
lymphatics which drain into the lymphatic trunks and the thoracic duct which  
ultimately drains into the venous circulation. The composition of the channels through  
which lymph passes is varied [Olszewski, W.L., in Olszewski, W.L. (ed), *Lymph*  
30 *Stasis: Pathophysiology, Diagnosis, and Treatment*. CRC Press: Boca Raton, Florida

(1991), pp. 235-258; and Kinmonth, J.B., in Kinmonth, J.B. (ed), *The Lymphatics: Diseases, Lymphography and Surgery*. Edward Arnold Publishers: London, England (1972), pp. 82-86], including the single endothelial layers of the initial lymphatics, the multiple layers of the collecting lymphatics including endothelium, muscular and adventitial layers, and the complex organization of the lymph node. The various organs of the body such as skin, lung, and GI tract have components of the lymphatics with various unique features. [See Ohkuma, M., in Olszewski (1991), *supra*, at pp. 157-190; Uhley, H. and Leeds, S., in Olszewski (1991), *supra*, at pp. 191-210; and Barrowman, J.A., in Olszewski (1991), at pp. 221-234).]

Molecular biology has identified at least a few genes and proteins postulated to have roles mediating the growth and/or embryonic development of the lymphatic system. One such gene/protein is the receptor tyrosine kinase designated Flt4 (fms-like tyrosine kinase 4), cloned from human erythroleukaemia cell and placental cDNA libraries. [See U.S. Patent No. 5,776,755; Aprelikova *et al.*, *Cancer Res.*, 52: 746-748 (1992); Galland *et al.*, *Genomics*, 13: 475-478 (1992); Galland *et al.*, *Oncogene*, 8: 1233-1240 (1993); and Pajusola *et al.*, *Cancer Res.*, 52:5738-5743 (1992), all incorporated herein by reference.] Studies showed that, in mouse embryos, a targeted disruption of the *Flt4* gene leads to a failure of the remodeling of the primary vascular network, and death after embryonic day 9.5 [Dumont *et al.*, *Science*, 282: 946-949 (1998)]. These studies suggested that *Flt4* has an essential role in the development of the embryonic vasculature, before the emergence of the lymphatic vessels. However, additional studies indicated that, during further development, the expression of *Flt4* becomes restricted mainly to lymphatic vessels [Kaipainen, *et al.*, *Proc. Natl. Acad. Sci. USA*, 92: 3566-3570 (1995)].

In humans, there are two isoforms of the Flt4 protein, designated as Flt4s (short, Genbank Accession No. X68203) and Flt4l (long, Genbank Accession Nos. X68203 and S66407, SEQ ID NO: 1). The sequence of these isoforms is largely identical, except for divergence that occurs at the carboxyl terminus of the receptor as a result of alternative mRNA splicing at the 3' end. The C-terminus of the long form contains three tyrosyl residues, and one of them (Y1337 (SEQ ID NO: 2)) serves as an autophosphorylation site in the receptor [Fournier *et al.*, *Oncogene*, 11: 921-931 (1995); and Pajusola, *et al.*, *Oncogene*, 8: 2931-2937 (1993)]. Only the long form is detected in human erythroleukaemia (HEL) and in a megakaryoblastic cell line (the

DAMI cells), and the mouse *Flt4* gene (Genbank Accession No. L07296) only produces one mRNA transcript, corresponding to Flt4l [Galland *et al.*, *Oncogene*, 8: 1233-1240 (1993); and Pajusola *et al.*, *Cancer Res.*, 52: 5738-5743 (1992)]. These findings suggest that the long form of Flt4 may be responsible for most of the biological properties of this receptor. The Flt4 protein is glycosylated and proteolytically processed in transfected cells [Pajusola *et al.*, *Oncogene*, 9: 3545-3555 (1994)]. During this process, the 175 kD form of the receptor matures to a 195 kD form, which is subsequently cleaved into a 125 kD C-terminal fragment, and a 75 kD extracellular domain-containing fragment, which are linked by disulphide bonding in the mature receptor.

Two growth factors, named vascular endothelial growth factors C and D (VEGF-C and VEGF-D) due to amino acid sequence similarity to earlier-discovered vascular endothelial growth factor, have been shown to bind and activate the tyrosine phosphorylation of Flt4. [Achen *et al.*, *Proc. Natl. Acad. Sci. USA*, 95: 548-553 (1998); Joukov *et al.*, *EMBO J.*, 15: 3898-3911; and Joukov *et al.*, *EMBO J.*, 15: 290-298 (1996)]. Because of Flt4's growth factor binding properties and the fact that Flt4 possesses amino acid sequence similarity to two previously identified VEGF receptors (Flt1/VEGFR-1 and KDR/VEGFR-2), Flt4 has also been designated VEGFR-3, and these terms are used interchangeably herein.

When VEGF-C was intentionally over-expressed under a basal keratin promoter in transgenic mice, a hyperplastic lymphatic vessel network in the skin was observed. [Jeltsch *et al.*, *Science*, 276:1423-1425 (1997).] The results of this study, when combined with the expression pattern of VEGFR-3 in the lymphatic vasculature, suggest that lymphatic growth may be induced by VEGF-C and mediated via VEGFR-3. Notwithstanding the foregoing insights involving one cell surface receptor and the two apparent ligands therefor, little is known about the developmental regulation of the lymphatic system.

Hereditary or primary lymphedema, first described by Milroy in 1892 [Milroy, *N.Y. Med. J.*, 56:505-508 (1892)], is a developmental disorder of the lymphatic system which leads to a disabling and disfiguring swelling of the extremities. Hereditary lymphedema generally shows an autosomal dominant pattern of inheritance with reduced penetrance, variable expression, and variable age-at-onset [Greenlee *et al.*, *Lymphology*, 26:156-168 (1993)]. Swelling may appear in one or all limbs,

varying in degree and distribution. If untreated, such swelling worsens over time. In rare instances, angiosarcoma may develop in affected tissues [Offori *et al.*, *Clin. Exp. Dermatol.*, 18:174-177 (1993)]. Despite having been described over a century ago, little progress has been made in understanding the mechanisms causing lymphedema.

5 A long-felt need exists for the identification of the presumed genetic variations that underlie hereditary lymphedema, to permit better informed genetic counseling in affected families, earlier diagnosis and treatment, and the development of more targeted and effective lymphedema therapeutic regimens. In addition, identification of genetic markers and high risk members of lymphedema families facilitates the  
10 identification and management of environmental factors that influence the expression and severity of a lymphedema phenotype.

### SUMMARY OF THE INVENTION

The present invention provides materials and methods that address one or more of the long-felt needs identified above by identifying a genetic marker that  
15 correlates and is posited to have a causative role in the development of hereditary lymphedema. The invention is based in part on the discovery that, in several families with members afflicted with hereditary lymphedema, the lymphedema phenotype correlates with genetic markers localized to chromosome 5q34-q35; and that in at least some such families, a missense mutation in the VEGFR-3 gene (which maps to  
20 chromosome 5q34-q35) exists that appears to behave in a loss-of-function dominant negative manner to decrease tyrosine kinase signaling of the receptor. In view of the fact that VEGFR-3 acts as a high affinity receptor for vascular endothelial growth factor C (VEGF-C), a growth factor whose effects include modulation of the growth of the lymphatic vascular network, these linkage and biochemical studies provide an  
25 important marker for determining a genetic predisposition for lymphedema in healthy individuals; and for diagnosing hereditary lymphedema in symptomatic individuals. Materials and methods for performing such genetic analyses are considered aspects of the present invention.

Thus, the invention provides genetic screening procedures that entail  
30 analyzing a person's genome -- in particular their *VEGFR-3* alleles -- to determine whether the individual possesses a genetic characteristic found in other individuals that are considered to be afflicted with, or at risk for, developing hereditary lymphedema.

For example, in one embodiment, the invention provides a method for determining a hereditary lymphedema development potential in a human subject comprising the steps of analyzing the coding sequence of the VEGFR-3 genes from the human subject; and determining hereditary lymphedema development potential in said human subject from the analyzing step.

In another embodiment, the invention provides a method of screening a human subject for an increased risk of developing a lymphatic disorder, comprising the steps of: (a) assaying nucleic acid of a human subject to determine a presence or an absence of a mutation altering the encoded VEGFR-3 amino acid sequence or expression of at least one VEGFR-3 allele; and (b) screening for an increased risk of developing a lymphatic disorder from the presence or absence of said mutation.

By "human subject" is meant any human being, human embryo, or human fetus. It will be apparent that methods of the present invention will be of particular interest to individuals that have themselves been diagnosed with lymphedema or have relatives that have been diagnosed with lymphedema.

By "screening for an increased risk" is meant determination of whether a genetic variation exists in the human subject that correlates with a greater likelihood of developing lymphedema than exists for the human population as a whole, or for a relevant racial or ethnic human sub-population to which the individual belongs. Both positive and negative determinations (i.e., determinations that a genetic predisposition marker is present or is absent) are intended to fall within the scope of screening methods of the invention. In preferred embodiments, the presence of a mutation altering the sequence or expression of at least one *Flt4* receptor tyrosine kinase allele in the nucleic acid is correlated with an increased risk of developing a lymphatic disorder, whereas the absence of such a mutation is reported as a negative determination.

By "lymphatic disorder" is meant any clinical condition affecting the lymphatic system, including but not limited to lymphedemas, lymphangiomas, lymphangiosarcomas, lymphangiomatosis, lymphangiectasis, and cystic hygroma. Preferred embodiments are methods of screening a human subject for an increased risk of developing a lymphedema disorder, i.e., any disorder that physicians would diagnose as lymphedema and that is characterized by swelling associated with lymph accumulation, other than lymphedemas for which non-genetic causes (e.g., parasites,

5 surgery) are known. By way of example, lymphedema disorders include Milroy-Nonne (OMIM 153100) syndrome-early onset lymphedema [Milroy, *N.Y. Med. J.*, 56:505-508 (1892); and Dale, *J. Med. Genet.*, 22: 274-278 (1985)] and lymphedema praecox (Meige syndrome, OMIM 153200)-late onset lymphedema [Lewis *et al.*, *J. Ped.*, 104:641-648 (1984); Holmes *et al.*, *Pediatrics* 61:575-579 (1978); and Wheeler *et al.*, *Plastic Reconstructive Surg.*, 67:362-364 (1981)] which generally are described as separate entities, both characterized by dominant inheritance. However, there is confusion in the literature about the separation of these disorders. In Milroy's syndrome, the presence of edema, which is usually more severe in the lower extremities, is seen from birth. Lymphedema praecox presents in a similar fashion but the onset of swelling is usually around puberty. Some cases have been reported to develop in the post-pubertal period. In the particular analyses described herein, the lymphedema families showing linkage to 5q34-q35 show an early onset for most affected individuals, but individuals in these pedigrees have presented during or after puberty.

15 The "assaying" step of the invention may involve any techniques available for analyzing nucleic acid to determine its characteristics, including but not limited to well-known techniques such as single-strand conformation polymorphism analysis (SSCP) [Orita *et al.*, *Proc Natl. Acad. Sci. USA*, 86: 2766-2770 (1989)]; heteroduplex analysis [White *et al.*, *Genomics*, 12: 301-306 (1992)]; denaturing gradient gel electrophoresis analysis [Fischer *et al.*, *Proc. Natl. Acad. Sci. USA*, 80: 1579-1583 (1983); and Riesner *et al.*, *Electrophoresis*, 10: 377-389 (1989)]; DNA sequencing; RNase cleavage [Myers *et al.*, *Science*, 230: 1242-1246 (1985)]; chemical cleavage of mismatch techniques [Rowley *et al.*, *Genomics*, 30: 574-582 (1995); and Roberts *et al.*, *Nucl. Acids Res.*, 25: 3377-3378 (1997)]; restriction fragment length polymorphism analysis; single nucleotide primer extension analysis [Shumaker *et al.*, *Hum. Mutat.*, 7: 346-354 (1996); and Pastinen *et al.*, *Genome Res.*, 7: 606-614 (1997)]; 5' nuclease assays [Pease *et al.*, *Proc. Natl. Acad. Sci. USA*, 91:5022-5026 (1994)]; DNA Microchip analysis [Ramsay, G., *Nature Biotechnology*, 16: 40-48 (1999); and Chee *et al.*, U.S. Patent No. 5,837,832]; and ligase chain reaction [Whiteley *et al.*, U.S. Patent No. 5,521,065]. [See generally, Schafer and Hawkins, *Nature Biotechnology*, 16: 33-39 (1998).] All of the foregoing documents are hereby incorporated by reference in their entirety.

In one preferred embodiment, the assaying involves sequencing of nucleic acid to determine nucleotide sequence thereof, using any available sequencing technique. [See, e.g., Sanger *et al.*, *Proc. Natl. Acad. Sci. (USA)*, 74: 5463-5467 (1977) (dideoxy chain termination method); Mirzabekov, *TIBTECH*, 12: 27-32 (1994) (sequencing by hybridization); Drmanac *et al.*, *Nature Biotechnology*, 16: 54-58 (1998); U.S. Patent No. 5,202,231; and *Science*, 260: 1649-1652 (1993) (sequencing by hybridization); Kieleczawa *et al.*, *Science*, 258: 1787-1791 (1992) (sequencing by primer walking); (Douglas *et al.*, *Biotechniques*, 14: 824-828 (1993) (Direct sequencing of PCR products); and Akane *et al.*, *Biotechniques* 16: 238-241 (1994); Maxam and Gilbert, *Meth. Enzymol.*, 65: 499-560 (1977) (chemical termination sequencing), all incorporated herein by reference.] The analysis may entail sequencing of the entire *VEGFR-3* gene genomic DNA sequence, or portions thereof; or sequencing of the entire *VEGFR-3* coding sequence or portions thereof. In some circumstances, the analysis may involve a determination of whether an individual possesses a particular *VEGFR-3* allelic variant, in which case sequencing of only a small portion of nucleic acid -- enough to determine the sequence of a particular codon characterizing the allelic variant -- is sufficient. This approach is appropriate, for example, when assaying to determine whether one family member inherited the same allelic variant that has been previously characterized for another family member, or, more generally, whether a person's genome contains an allelic variant that has been previously characterized and correlated with heritable lymphedema. More generally, the sequencing may be focused on those portions of the *VEGFR-3* sequence that encode a *VEGFR-3* kinase domain, since several different and apparently causative mutations in affected individuals that have been identified correspond to residues within an intracellular *VEGFR-3* kinase domain. Referring to SEQ ID NOs: 1 and 2, the two kinase domains of human wild type *VEGFR-3* correspond to nucleotides 2546 to 2848 and 3044 to 3514 of SEQ ID NO: 1, which encode residues 843 to 943 and 1009 to 1165 of SEQ ID NO: 2. Such kinase domains are localized to exons 17-20 and 22-26 in the *VEGFR-3* gene, so the sequencing/analysis may be focused on those exons in particular. Molecular modeling suggests that, within these domains, residues G852, G854, G857, K879, E896, H1035, D1037, N1042, D1055, F1056, G1057, E1084, D1096, and R1159 are of particular importance in comprising or shaping the catalytic pocket of the *VEGFR-3* kinase domains, so the sequencing may focus on



these residues (in addition to residues described herein for which mutations have already been identified).

In a related embodiment, the invention provides PCR primers useful for amplifying particular exon sequences of human VEGFR-3 genomic DNA. The Examples below identify preferred primers for amplifying Exon 17, Exon 22, and Exon 24 sequences, where specific missense mutations described herein map. In addition, the Examples below describe the Exon-Intron junctions of human VEGFR-3, which, in combination with the VEGFR-3 cDNA sequence provided herein, permit the manufacture of appropriate oligonucleotide primers for other exons. Any such primers of, *e.g.*, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, or more nucleotides that are identical or exactly complementary to a human VEGFR-3 genomic sequence and that includes or is within 50 nucleotides of a VEGFR-3 exon-intron splice site is intended to be within the scope of the invention.

In another embodiment, the assaying step comprises performing a hybridization assay to determine whether nucleic acid from the human subject has a nucleotide sequence identical to or different from one or more reference sequences. In a preferred embodiment, the hybridization involves a determination of whether nucleic acid derived from the human subject will hybridize with one or more oligonucleotides, wherein the oligonucleotides have nucleotide sequences that correspond identically to a portion of the VEGFR-3 gene sequence, preferably the VEGFR-3 coding sequence set forth in SEQ ID NO: 1, or that correspond identically except for one mismatch. The hybridization conditions are selected to differentiate between perfect sequence complementarity and imperfect matches differing by one or more bases. Such hybridization experiments thereby can provide single nucleotide polymorphism sequence information about the nucleic acid from the human subject, by virtue of knowing the sequences of the oligonucleotides used in the experiments.

Several of the techniques outlined above involve an analysis wherein one performs a polynucleotide migration assay, *e.g.*, on a polyacrylamide electrophoresis gel, under denaturing or non-denaturing conditions. Nucleic acid derived from the human subject is subjected to gel electrophoresis, usually adjacent to one or more reference nucleic acids, such as reference VEGFR-3 sequences having a coding sequence identical to all or a portion of SEQ ID NO: 1, or identical except for

one known polymorphism. The nucleic acid from the human subject and the reference sequence(s) are subjected to similar chemical or enzymatic treatments and then electrophoresed under conditions whereby the polynucleotides will show a differential migration pattern, unless they contain identical sequences. [See generally Ausubel *et al.* (eds.), *Current Protocols in Molecular Biology*, New York: John Wiley & Sons, Inc. (1987-1999); and Sambrook *et al.*, (eds.), *Molecular Cloning, A Laboratory Manual*, Cold Spring Harbor, New York: Cold Spring Harbor Laboratory Press (1989), both incorporated herein by reference in their entirety.]

In the context of assaying, the term "nucleic acid of a human subject" is intended to include nucleic acid obtained directly from the human subject (*e.g.*, DNA or RNA obtained from a biological sample such as a blood, tissue, or other cell or fluid sample); and also nucleic acid derived from nucleic acid obtained directly from the human subject. By way of non-limiting examples, well known procedures exist for creating cDNA that is complementary to RNA derived from a biological sample from a human subject, and for amplifying (*e.g.*, via polymerase chain reaction (PCR)) DNA or RNA derived from a biological sample obtained from a human subject. Any such derived polynucleotide which retains relevant nucleotide sequence information of the human subject's own DNA/RNA is intended to fall within the definition of "nucleic acid of a human subject" for the purposes of the present invention.

In the context of assaying, the term "mutation" includes addition, deletion, and/or substitution of one or more nucleotides in the *VEGFR-3* gene sequence. The invention is demonstrated by way of non-limiting examples set forth below that identify several mutations in *VEGFR-3*, including single nucleotide polymorphisms that introduce missense mutations into the *VEGFR-3* coding sequence (as compared to the *VEGFR-3* cDNA sequence set forth in SEQ ID NO: 1) and other polymorphisms that occur in introns and that are identifiable via sequencing, restriction fragment length polymorphism, or other techniques. Example 2 provides an assay to determine whether a *VEGFR-3* mutation inhibits VEGFR-3 signaling. Additional assays to study both ligand binding and signaling activities of VEGFR-3 are disclosed, *e.g.*, in U.S. Patent No. 5,776,755 and International Patent Publication No. WO 98/33917, published 06 August 1998, both of which are incorporated herein by reference in their entirety. Evidence that a VEGFR-3 mutation inhibits VEGFR-3 signaling is evidence that the mutation may have a causative role in lymphedema

phenotype. However, even mutations that have no apparent causative role may serve as useful markers for heritable lymphedema, provided that the appearance of the mutation correlates reliably with the appearance of lymphedema.

In a related embodiment, the invention provides a method of screening  
5 for a VEGFR-3 hereditary lymphedema genotype in a human subject, comprising the steps of: (a) providing a biological sample comprising nucleic acid from a human subject; (b) analyzing the nucleic acid for the presence of a mutation or mutations in a VEGFR-3 allele in the nucleic acid of the human subject; (c) determining a VEGFR-3 genotype from said analyzing step; and (d) correlating the presence of a mutation in a  
10 VEGFR-3 allele with a hereditary lymphedema genotype. In a preferred embodiment, the biological sample is a cell sample containing human cells that contain genomic DNA of the human subject.

Although more time consuming and expensive than methods involving nucleic acid analysis, the invention also may be practiced by assaying protein of a  
15 human subject to determine the presence or absence of an amino acid sequence variation in VEGFR-3 protein from the human subject. Such protein analyses may be performed, e.g., by fragmenting VEGFR-3 protein via chemical or enzymatic methods and sequencing the resultant peptides; or by Western analyses using an antibody having specificity for a particular allelic variant of VEGFR-3.

20 The invention also provides materials that are useful for performing methods of the invention. For example, the present invention provides oligonucleotides useful as probes in the many analyzing techniques described above. In general, such oligonucleotide probes comprise 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38,  
25 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 nucleotides that have a sequence that is identical, or exactly complementary, to a portion of a human VEGFR-3 gene sequence, or that is identical or exactly complementary except for one nucleotide substitution. In a preferred embodiment, the oligonucleotides have a sequence that corresponds in the foregoing manner to a human VEGFR-3 coding sequence, and in  
30 particular, the VEGFR-3 coding sequence set forth in SEQ ID NO: 1. In one variation, an oligonucleotide probe of the invention is purified and isolated. In another variation, the oligonucleotide probe is labeled, e.g., with a radioisotope, chromophore,

or fluorophore. In yet another variation, the probe is covalently attached to a solid support. [See generally Ausubel *et al.* And Sambrook *et al.*, *supra.*]

In preferred embodiments, the invention comprises an oligonucleotide probe useful for detecting one or more of several mutations that have been characterized herein in affected individuals, including:

- (1) a missense mutation at nucleotide 3360 of SEQ ID NO: 1, causing a proline to leucine change at residue 1114 in SEQ ID NO: 2;
- (2) a missense mutation at nucleotide 2588 of SEQ ID NO: 1, causing a glycine to arginine change at residue 857 in SEQ ID NO: 2;
- (3) a missense mutation at nucleotide 3141 of SEQ ID NO: 1, causing an arginine to proline change at residue 1041 in SEQ ID NO: 2;
- (4) a missense mutation at nucleotide 3150 in SEQ ID NO: 1, causing a leucine to proline change at residue 1044 in SEQ ID NO: 2; and
- (5) a missense mutation at nucleotide 3164 of SEQ ID NO: 1, causing an aspartic acid to asparagine change at residue 1049 in SEQ ID NO: 2.

For example, the invention provides oligonucleotides comprising anywhere from 6 to 50 nucleotides that have a sequence that is identical to, or exactly complementary to, a portion of the human VEGFR-3 coding sequence set forth in SEQ ID NO: 1, except for a nucleotide substitution corresponding to nucleotide 3360 of SEQ ID NO: 1.

Such oligonucleotides may be generically described by the formula  $X_nYZ_m$  or its complement; where  $n$  and  $m$  are integers from 0 to 49; where  $5 \leq (n + m) \leq 49$ ; where  $X_n$  is a stretch of  $n$  nucleotides identical to a first portion of SEQ ID NO: 1 and  $Z_m$  is a stretch of  $m$  nucleotides identical to a second portion of SEQ ID NO: 1, wherein the first and second portions are separated in SEQ ID NO: 1 by one nucleotide; and wherein  $Y$  represents a nucleotide other than the nucleotide that separates the first and second portions of SEQ ID NO: 1. For example, where  $X_n$  represents 0 to 49 nucleotides immediately upstream (5') of nucleotide 3360 of SEQ ID NO: 1 and  $Z_m$  represents 0 to 49 nucleotides immediately downstream (3') of nucleotide 3360 of SEQ ID NO: 1,  $Y$  represents a nucleotide other than cytosine, since a cytosine nucleotide is found at position 3360 of SEQ ID NO: 1. In a preferred embodiment,  $Y$  is a thymine nucleotide. Similar examples are contemplated for the other specific mutations identified immediately above.

In a related embodiment, the invention provides a kit comprising at least two such oligonucleotide probes. Preferably, the two or more probes are provided in separate containers, or attached to separate solid supports, or attached separately to the same solid support, e.g., on a DNA microchip.

5 In still another related embodiment, the invention provides an array of oligonucleotide probes immobilized on a solid support, the array having at least 4 probes, preferably at least 100 probes, and preferably up to 100,000, 10,000, or 1000 probes, wherein each probe occupies a separate known site in the array. In a preferred embodiment, the array includes probe sets comprising two to four probes, wherein one  
10 probe is exactly identical or exactly complementary to a human VEGFR-3 coding sequence, and the other one to three members of the set are exactly identical to the first member, but for at least one different nucleotide, which different nucleotide is located in the same position in each of the one to three additional set members. In one preferred embodiment, the array comprises several such sets of probes, wherein the  
15 sets correspond to different segments of the human VEGFR-3 gene sequence. In a highly preferred embodiment, the array comprises enough sets of oligonucleotides of length N to correspond to every particular N-mer sequence of the VEGFR-3 gene, where N is preferably 6 to 25 and more preferably 9 to 20. Materials and methods for making such probes are known in the art and are described, for example, in U.S. Patent  
20 Nos. 5,837,832, 5,202,231, 5,002,867, and 5,143,854.

Moreover, the discoveries which underlie the present invention identify a target for therapeutic intervention in cases of hereditary lymphedema. The causative mutations in the families that have been studied in greatest detail are mutations that appear to result in VEGFR-3 signaling that is reduced in heterozygous affected  
25 individuals, but not completely eliminated. This data supports a therapeutic indication for administration of agents, such as VEGFR-3 ligand polypeptides, that will induce VEGFR-3 signaling in the lymphatic endothelia of affected individuals to effect improvement in the structure and function of the lymphatic vasculature of such individuals. In addition, therapeutic gene therapy, to replace defective VEGFR-3  
30 alleles or increase production of VEGFR-3 ligand polypeptides *in vivo*, is envisioned as an aspect of the invention.

Thus, in yet another aspect, the invention provides a therapeutic or prophylactic method of treatment for lymphedema, comprising the step of

administering to a mammalian subject in need of therapeutic or prophylactic treatment for lymphedema a composition comprising a compound effective to induce intracellular signaling of VEGFR-3 in lymphatic endothelial cells that express said receptor. In a preferred embodiment, the compound comprises a polypeptide ligand for VEGFR-3,  
5 or a polynucleotide encoding such a ligand, wherein the polynucleotide is administered in a form that results in transcription and translation of the polynucleotide in the mammalian subject to produce the ligand *in vivo*. In another preferred embodiment, the compound comprises any small molecule that is capable of binding to the VEGFR-3 receptor extracellular or intracellular domain and inducing intracellular signaling.

10 For example, the invention provides a therapeutic or prophylactic method of treatment for lymphedema, comprising the step of administering to a mammalian subject in need of therapeutic or prophylactic treatment for lymphedema a composition comprising a polynucleotide, the polynucleotide comprising a nucleotide sequence that encodes a vascular endothelial growth factor C (VEGF-C) polypeptide.  
15 In a preferred embodiment, the subject is a human subject.

While it is contemplated that the VEGF-C polynucleotide could be administered purely as a prophylactic treatment to prevent lymphedema in subjects at risk for developing lymphedema, it is contemplated in a preferred embodiment that the polynucleotide be administered to subjects afflicted with lymphedema, for the purpose  
20 of ameliorating its symptoms (e.g., swelling due to the accumulation of lymph). The polynucleotide is included in the composition in an amount and in a form effective to promote expression of a VEGF-C polypeptide in or near the lymphatic endothelia of the mammalian subject, to stimulate VEGFR-3 signaling in the lymphatic endothelia of the subject.

25 In a preferred embodiment, the mammalian subject is a human subject. Practice of methods of the invention in other mammalian subjects, especially mammals that are conventionally used as models for demonstrating therapeutic efficacy in humans (e.g., primate, porcine, canine, equine, murine, or rabbit animals), also is contemplated. Several potential animal models for hereditary lymphedema have been  
30 described in the literature. [See, e.g., Lyon *et al.*, *Mouse News Lett.* 71: 26 (1984), *Mouse News Lett.* 74: 96 (1986), and *Genetic variants and strains of the laboratory mouse*, 2nd ed., New York: Oxford University Press (1989), p. 70 (*Chylous ascites mouse*); Dumont *et al.*, *Science*, 282: 946-949 (1998) (heterozygous VEGFR-3

knockout mouse); Patterson *et al.*, "Hereditary Lymphedema," *Comparative Pathology Bulletin*, 3: 2 (1971) (canine hereditary lymphedema model); van der Putte, "Congenital Hereditary Lymphedema in the Pig," *Lympho*, 11: 1-9 (1978); and Campbell-Beggs *et al.*, "Chyloabdomen in a neonatal foal," *Veterinary Record*, 137: 96-98 (1995).] Those models which are determined to have analogous mutations to the VEGFR-3 gene, such as the *Chylous ascetei* (*Chy*) mouse, are preferred. The present inventors have analyzed the *VEGFR-3* genes of the *Chy* mouse and determined that affected mice contain a missense mutation that results in a phenylalanine (rather than an isoleucine) in the VEGFR-3 sequence at a position corresponding to the isoleucine at position 1053 of SEQ ID NO: 2. This mutation maps to the catalytic pocket region of the tyrosine kinase domain of the VEGFR-3 protein, and may represent a viable model for identical mutations in human (if discovered) or other mutations in humans that similarly affect the tyrosine kinase catalytic domain. The *Chy* mouse has peripheral swelling (oedema) after birth and chyle ascites. In another embodiment, "knock in" homologous recombination genetic engineering strategies are used to create an animal model (e.g., a mouse model) having a VEGFR-3 allelic variation analogous to the human variations described herein. [See, e.g., Partanen *et al.*, *Genes & Development*, 12: 2332-2344 (1998) (gene targeting to introduce mutations into a receptor protein (FGFR-1) in mice).] Such mice can also be bred to the heterozygous VEGFR-3 knockout mice or *Chy* mice described above to further modify the phenotypic severity of the lymphedema disease.

For the practice of methods of the invention, the term "VEGF-C polypeptide" is intended to include any polypeptide that has a VEGF-C or VEGF-C analog amino acid sequence (as defined elsewhere herein in greater detail) and that is able to bind the VEGFR-3 extracellular domain and stimulate VEGFR-3 signaling *in vivo*. The term "VEGF-C polynucleotide" is intended to include any polynucleotide (e.g., DNA or RNA, single- or double-stranded) comprising a nucleotide sequence that encodes a VEGF-C polypeptide. Due to the well-known degeneracy of the genetic code, multiple VEGF-C polynucleotide sequences exist that encode any selected VEGF-C polypeptide. Preferred VEGF-C polynucleotides, polypeptides, and VEGF-C variants and analogs for use in this invention are disclosed in International Patent Application No. PCT/US98/01973, published as WO 98/33917, incorporated herein by reference in its entirety.

For treatment of humans, VEGF-C polypeptides with an amino acid sequence of a human VEGF-C are highly preferred, and polynucleotides comprising a nucleotide sequence of a human VEGF-C cDNA are highly preferred. By "human VEGF-C" is meant a polypeptide corresponding to a naturally occurring protein (prepro-protein, partially-processed protein, or fully-processed mature protein) encoded by any allele of the human VEGF-C gene, or a polypeptide comprising a biologically active fragment of a naturally-occurring mature protein. By way of example, a human VEGF-C comprises a continuous portion of the amino acid sequence set forth in SEQ ID NO: 4 sufficient to permit the polypeptide to bind and stimulate VEGFR-3 phosphorylation in cells that express such receptors. A polypeptide comprising amino acids 131-211 of SEQ ID NO: 4 is specifically contemplated. For example, polypeptides having an amino acid sequence comprising a continuous portion of SEQ ID NO: 4, the continuous portion having, as its amino terminus, an amino acid selected from the group consisting of positions 30-131 of SEQ ID NO: 4, and having, as its carboxyl terminus, an amino acid selected from the group consisting of positions 211-419 of SEQ ID NO: 4 are contemplated. An amino terminus selected from the group consisting of positions 102-131 of SEQ ID NO: 4 is preferred, and an amino terminus selected from the group consisting of positions 103-113 of SEQ ID NO: 4 is highly preferred. Likewise, a carboxyl terminus selected from the group consisting of positions 211-227 of SEQ ID NO: 4 is preferred. As stated above, the term "human VEGF-C" also is intended to encompass polypeptides encoded by allelic variants of the human VEGF-C characterized by the sequences set forth in SEQ ID NOs: 3 & 4.

Moreover, since the therapeutic VEGF-C is to be administered as recombinant VEGF-C or indirectly via somatic gene therapy, it is within the skill in the art to make and use analogs of human VEGF-C (and polynucleotides that encode such analogs) wherein one or more amino acids have been added, deleted, or replaced with other amino acids, especially with conservative replacements, and wherein the VEGFR-3-stimulatory biological activity has been retained. Analogs that retain VEGFR-3-stimulatory VEGF-C biological activity are contemplated as VEGF-C polypeptides for use in the present invention. In a preferred embodiment, analogs having 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 such modifications and that retain VEGFR-3-stimulatory VEGF-C biological



activity are contemplated as VEGF-C polypeptides for use in the present invention. Analogs having a deletion of or substitution for the cysteine residue at position 156 of SEQ ID NO: 4 and that retain VEGFR-3 stimulatory activity but have reduced activity toward the receptor VEGFR-2, which is expressed in blood vessels, are specifically contemplated. See WO 98/33917. Polynucleotides encoding such analogs are generated using conventional PCR, site-directed mutagenesis, and chemical synthesis techniques.

Also contemplated as VEGF-C polypeptides are non-human mammalian or avian VEGF-C polypeptides and polynucleotides. By "mammalian VEGF-C" is meant a polypeptide corresponding to a naturally occurring protein (prepro-protein, partially-processed protein, or fully-processed mature protein) encoded by any allele of a VEGF-C gene of any mammal, or a polypeptide comprising a biologically active fragment of a mature protein. The term "mammalian VEGF-C polypeptide" is intended to include analogs of mammalian VEGF-C's that possess the *in vivo* VEGFR-3-stimulatory effects of the mammalian VEGF-C.

Irrespective of which encoded VEGF-C polypeptide is chosen, any VEGF-C polynucleotide gene therapy pharmaceutical encoding it preferably comprises a nucleotide sequence encoding a secretory signal peptide fused in-frame with the VEGF-C polypeptide sequence. The secretory signal peptide directs secretion of the VEGF-C polypeptide by the cells that express the polynucleotide, and is cleaved by the cell from the secreted VEGF-C polypeptide. For example, the VEGF-C polynucleotide could encode the complete prepro-VEGF-C sequence set forth in SEQ ID NO: 4; or could encode the VEGF-C signal peptide fused in-frame to a sequence encoding a fully-processed VEGF-C (e.g., amino acids 103-227 of SEQ ID NO: 4) or VEGF-C analog. Moreover, there is no requirement that the signal peptide be derived from VEGF-C. The signal peptide sequence can be that of another secreted protein, or can be a completely synthetic signal sequence effective to direct secretion in cells of the mammalian subject.

In one embodiment, the VEGF-C polynucleotide of the invention comprises a nucleotide sequence that will hybridize to a polynucleotide that is complementary to the human VEGF-C cDNA sequence specified in SEQ ID NO: 3 under the following exemplary stringent hybridization conditions: hybridization at 42°C in 50% formamide, 5X SSC, 20 mM Na<sub>2</sub>PO<sub>4</sub>, pH 6.8; and washing in 1X SSC at

55°C for 30 minutes; and wherein the nucleotide sequence encodes a polypeptide that binds and stimulates human VEGFR-3. It is understood that variation in these exemplary conditions occur based on the length and GC nucleotide content of the sequences to be hybridized. Formulas standard in the art are appropriate for determining appropriate hybridization conditions. [See Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual* (Second ed., Cold Spring Harbor, New York: Cold Spring Harbor Laboratory Press, 1989) §§ 9.47-9.51.]

In preferred embodiments, the VEGF-C polynucleotide further comprises additional sequences to facilitate the VEGF-C gene therapy. In one embodiment, a "naked" VEGF-C transgene (i.e., a transgene without a viral, liposomal, or other vector to facilitate transfection) is employed for gene therapy. In this embodiment, the VEGF-C polynucleotide preferably comprises a suitable promoter and/or enhancer sequence (e.g., cytomegalovirus promoter/enhancer [Lehner *et al.*, *J. Clin. Microbiol.*, 29:2494-2502 (1991); Boshart *et al.*, *Cell*, 41:521-530 (1985)]; Rous sarcoma virus promoter [Davis *et al.*, *Hum. Gene Ther.*, 4:151 (1993)]; Tie promoter [Korhonen *et al.*, *Blood*, 86(5): 1828-1835 (1995)]; or simian virus 40 promoter) for expression in the target mammalian cells, the promoter being operatively linked upstream (i.e., 5') of the VEGF-C coding sequence. The VEGF-C polynucleotide also preferably further includes a suitable polyadenylation sequence (e.g., the SV40 or human growth hormone gene polyadenylation sequence) operably linked downstream (i.e., 3') of the VEGF-C coding sequence. The polynucleotide may further optionally comprise sequences whose only intended function is to facilitate large-scale production of the vector, e.g., in bacteria, such as a bacterial origin of replication and a sequence encoding a selectable marker. However, in a preferred embodiment, such extraneous sequences are at least partially cleaved off prior to administration to humans according to methods of the invention. One can manufacture and administer such polynucleotides to achieve successful gene therapy using procedures that have been described in the literature for other transgenes. See, e.g., Isner *et al.*, *Circulation*, 91: 2687-2692 (1995); and Isner *et al.*, *Human Gene Therapy*, 7: 989-1011 (1996); incorporated herein by reference in the entirety.

Any suitable vector may be used to introduce the VEGF-C transgene into the host. Exemplary vectors that have been described in the literature include replication-deficient retroviral vectors, including but not limited to lentivirus vectors

[Kim *et al.*, *J. Virol.*, 72(1): 811-816 (1998); Kingsman & Johnson, *Scrip Magazine*, October, 1998, pp. 43-46.]; adeno-associated viral vectors [Gnatenko *et al.*, *J. Investig. Med.*, 45: 87-98 (1997)]; adenoviral vectors [See, *e.g.*, U.S. Patent No. 5,792,453; Quantin *et al.*, *Proc. Natl. Acad. Sci. USA*, 89: 2581-2584 (1992);  
5 Stratford-Perricadet *et al.*, *J. Clin. Invest.*, 90: 626-630 (1992); and Rosenfeld *et al.*, *Cell*, 68: 143-155 (1992)]; Lipofectin-mediated gene transfer (BRL); liposomal vectors [See, *e.g.*, U.S. Patent No. 5,631,237 (Liposomes comprising Sendai virus proteins)] ; and combinations thereof. All of the foregoing documents are incorporated herein by reference in the entirety. Replication-deficient adenoviral vectors constitute a  
10 preferred embodiment.

In embodiments employing a viral vector, preferred polynucleotides still include a suitable promoter and polyadenylation sequence as described above. Moreover, it will be readily apparent that, in these embodiments, the polynucleotide further includes vector polynucleotide sequences (*e.g.*, adenoviral polynucleotide  
15 sequences) operably connected to the sequence encoding a VEGF-C polypeptide.

Thus, in one embodiment the composition to be administered comprises a vector, wherein the vector comprises the VEGF-C polynucleotide. In a preferred embodiment, the vector is an adenovirus vector. In a highly preferred embodiment, the adenovirus vector is replication-deficient, *i.e.*, it cannot replicate in the mammalian  
20 subject due to deletion of essential viral-replication sequences from the adenoviral genome. For example, the inventors contemplate a method wherein the vector comprises a replication-deficient adenovirus, the adenovirus comprising the VEGF-C polynucleotide operably connected to a promoter and flanked on either end by adenoviral polynucleotide sequences.

The composition to be administered according to methods of the invention preferably comprises (in addition to the polynucleotide or vector) a pharmaceutically-acceptable carrier solution such as water, saline, phosphate-buffered saline, glucose, or other carriers conventionally used to deliver therapeutics intravascularly. Multi-gene therapy is also contemplated, in which case the  
25 composition optionally comprises both the VEGF-C polynucleotide/vector and another polynucleotide/vector. As described in greater detail below, a VEGF-D transgene is a preferred candidate for co-administration with the VEGF-C transgene.  
30

The "administering" that is performed according to the present method may be performed using any medically-accepted means for introducing a therapeutic directly or indirectly into a mammalian subject to reach the lymph or the lymphatic system, including but not limited to injections; oral ingestion; intranasal or topical administration; and the like. In a preferred embodiment, administration of the composition comprising the VEGF-C polynucleotide is performed intravascularly, such as by intravenous or intra-arterial injection, or by subcutaneous injection or local depot administration. In a highly preferred embodiment, the composition is administered locally, *e.g.*, to the site of swelling.

In still another variation, endothelial cells or endothelial progenitor cells are transfected *ex vivo* with a wild type VEGFR-3 transgene, and the transfected cells are administered to the mammalian subject.

In another aspect, the invention provides a therapeutic or prophylactic method of treating for lymphedema, comprising the step of administering to a mammalian subject in need of treatment for lymphedema a composition comprising a VEGF-C polypeptide, in an amount effective to treat or prevent swelling associated with lymphedema. Administration via one or more intravenous or subcutaneous injections is contemplated. Co-administration of VEGF-C polynucleotides and VEGF-C polypeptides is also contemplated.

In yet another embodiment, the invention provides the use of a VEGF-C polynucleotide or VEGF-C polypeptide for the manufacture of a medicament for the treatment or prevention of lymphedema.

In still another embodiment, the invention provides a therapeutic or prophylactic method of treatment for lymphedema, comprising the step of administering to a mammalian subject in need of therapeutic or prophylactic treatment of lymphedema a composition comprising a polynucleotide, the polynucleotide comprising a nucleotide sequence that encodes a vascular endothelial growth factor D (VEGF-D) polypeptide. Such methods are practiced essentially as described herein with respect to VEGF-C-encoding polynucleotides, except that polynucleotides encoding VEGF-D are employed. A detailed description of the human VEGF-D gene and protein are provided in Achen, *et al.*, *Proc. Nat'l Acad. Sci. U.S.A.*, 95(2): 548-553 (1998); International Patent Publication No. WO 98/07832, published 26 February 1998; and in Genbank Accession No. AJ000185, all incorporated herein by reference.

A cDNA and deduced amino acid sequence for prepro-VEGF-D is set forth herein in SEQ ID NOs: 5 and 6. Of course, due to the well-known degeneracy of the genetic code, multiple VEGF-D encoding polynucleotide sequence exist, any of which may be employed according to the methods taught herein.

5                   As described herein in detail with respect to VEGF-C, the use of polynucleotides that encode VEGF-D fragments, VEGF-D analogs, VEGF-D allelic and interspecies variants, and the like which possess *in vivo* stimulatory effects of human VEGF-D are all contemplated as being encompassed by the present invention.

10                   In yet another embodiment, the invention provides a therapeutic or prophylactic method of treatment for lymphedema, comprising the step of administering to a mammalian subject in need of treatment for lymphedema a composition comprising a VEGF-D polypeptide, in an amount effective to treat or prevent swelling associated with lymphedema. Administration via one or more intravenous or subcutaneous injections is contemplated.

15                   The VEGFR-3 allelic variant polynucleotides and polypeptides described herein that were discovered and characterized by the present inventors are themselves considered aspects of the invention. Such polynucleotides and polypeptides are useful, for example, in screening assays (*e.g.*, cell-based assays or assays involving transgenic mice that express the polynucleotide in lieu of a native VEGF-3 allele) to study the biological activities of VEGFR-3 variant alleles and  
20                   identify compounds that are capable of modulating that activity, *e.g.*, to identify therapeutic candidates for treatment of lymphedema. Such screening assays are also considered aspects of the invention.

25                   The polypeptides of the invention are intended to include complete VEGFR-3 polypeptides with signal peptide (*e.g.*, approximately residues 1 to 20 of SEQ ID NO: 2), mature VEGFR-3 polypeptides lacking any signal peptide, and recombinant variants wherein a foreign or synthetic signal peptide has been fused to the mature VEGFR-3 polypeptide. Polynucleotides of the invention include all polynucleotides that encode all such polypeptides. It will be understood that for  
30                   essentially any polypeptide, many polynucleotides can be constructed that encode the polypeptide by virtue of the well known degeneracy of the genetic code. All such polynucleotides are intended as aspects of the invention.

Thus, in yet another aspect, the invention provides a purified polynucleotide comprising a nucleotide sequence encoding a human VEGFR-3 protein variant, wherein said polynucleotide is capable of hybridizing to the complement of SEQ ID NO: 1 under stringent hybridization conditions, and wherein the encoded VEGFR-3 protein variant has an amino acid sequence that differs at position 1114, 857, 1041, 1044 or 1049 from the amino acid sequence set forth in SEQ ID NO: 1. Exemplary conditions are as follows: hybridization at 42°C in 50% formamide, 5X SSC, 20 mM Na•PO<sub>4</sub>, pH 6.8; and washing in 0.2X SSC at 55°C. It is understood by those of skill in the art that variation in these conditions occurs based on the length and GC nucleotide content of the sequences to be hybridized. Formulas standard in the art are appropriate for determining appropriate hybridization conditions. [See Sambrook et al. (1989), *supra*, §§ 9.47-9.51.]

In a related embodiment, the invention provides a purified polynucleotide comprising a nucleotide sequence encoding a VEGFR-3 protein of a human that is affected with heritable lymphedema or other lymphatic disorder; wherein the polynucleotide is capable of hybridizing to the complement of SEQ ID NO: 1 under stringent hybridization conditions, and wherein the encoded polynucleotide has an amino acid sequence that differs from SEQ ID NO: 1 at at least one codon. It will be understood that conventional recombinant techniques can be used to isolate such polynucleotides from individuals affected with heritable lymphedema or their relatives. The wildtype VEGFR-3 cDNA sequence set forth in SEQ ID NO: 1 (or its complement, or fragments thereof) is used as a probe to identify and isolate VEGFR-3 sequences from nucleic acid derived from the individuals. Alternatively, PCR amplification primers based on the wildtype VEGFR-3 sequence are generated and used to amplify either VEGFR-3 genomic DNA or VEGFR-3 mRNA from the human subject. The resultant amplified genomic DNA or cDNA is sequenced to determine the variations that characterize the VEGFR-3 lymphedema allele of the individual. Preferred VEGFR-3 lymphedema alleles include, but are not limited to the P1114L, G857R, R1041P, L1044P and D1049N alleles described in detail herein.

In addition, the invention provides vectors that comprise the polynucleotides of the invention. Such vectors are useful for amplifying and expressing the VEGFR-3 proteins encoded by the polynucleotides, and for creating recombinant host cells and/or transgenic animals that express the polynucleotides. The

invention further provides a host cell transformed or transfected with polynucleotides (including vectors) of the invention. In a preferred embodiment, the host cell expresses the encoded VEGFR-3 protein on its surface. Such host cells are useful in cell-based screening assays for identifying modulators that stimulate or inhibit signaling of the encoded VEGFR-3. Modulators that stimulate VEGFR-3 signaling have utility as therapeutics to treat lymphedemas, whereas modulators that are inhibitory have utility for treating hyperplastic lymphatic conditions mediated by the allelic variant VEGFR-3. In a preferred embodiment, host cells of the invention are co-transfected with both a wildtype and an allelic variant VEGFR-3 polynucleotide, such that the cells express both receptor types on their surface. Such host cells are preferred for simulating a heterozygous VEGFR-3 genotype of many individuals affected with lymphedema.

In yet another aspect, the invention provides a transgenic mammal, e.g., mouse, characterized by a non-native VEGFR-3 allele that has been introduced into the mouse, and the transgenic progeny thereof. Preferred allelic variants include allelic variants that correlate with hereditary lymphedema in human subjects, such as an allelic variant wherein a P1114L, G857R, R1041P, L1044P or D1049N missense mutation has been introduced into the murine VEGFR-3 gene, or wherein the human P1114L, G857R, R1041P, L1044P or D1049N allelic variant has been substituted for a murine VEGFR-3 allele. Such mice are produced using standard methods. [See, e.g., Hogan *et al.* (eds.), *Manipulating the Mouse Embryo*, Cold Spring Harbor, New York: Cold Spring Harbor Laboratory (1986).] The introduction of the human-like mutations into non-human sequences is readily achieved with standard techniques, such as site-directed mutagenesis. The determination of which residues in a non-human sequence to alter to mimic the foregoing human mutations is routine since the foregoing mutations all occur in regions of the VEGFR-3 sequence that contain residues that are highly conserved between species. See Figs. 3A-3B.

In yet another aspect, the invention provides assays for identifying modulators of VEGFR-3 signaling, particularly modulators of the signaling of allelic variants of VEGFR-3 that correlate with lymphatic disorders such as heritable lymphedema. For example, the invention provides a method for identifying a modulator of intracellular VEGFR-3 signaling, comprising the steps of: contacting a cell expressing at least one mutant mammalian VEGFR-3 polypeptide in the presence and in the absence of a putative modulator compound; b) detecting VEGFR-3

signaling in the cell; and c) identifying a putative modulator compound in view of decreased or increased signaling in the presence of the putative modulator, as compared to signaling in the absence of the putative modulator.

By "mutant mammalian VEGFR-3 polypeptide" is meant a VEGFR-3 polypeptide that varies from a wildtype mammalian VEGFR-3 polypeptide (e.g., by virtue of one or more amino acid additions, deletions, or substitutions), wherein the variation is reflective of a naturally occurring variation that has been correlated with a lymphatic disorder, such as lymphedema. By way of example, the previously described substitution variations of human VEGFR-3, such as P1114L, have been correlated with heritable lymphedema. Any of the human allelic variants described above, or analogous human allelic variants having a different substitution at the indicated amino acid positions, or a non-human VEGFR-3 into which a mutation at the position corresponding to any of the described positions has been introduced are all examples of mutant mammalian VEGFR-3 polypeptides.

The detecting step can entail the detection of any parameter indicative of VEGFR-3 signaling. For example, the detecting step can entail a measurement of VEGFR-3 autophosphorylation, or a measurement of VEGFR-3-mediated cell growth, or a measurement of any step in the VEGFR-3 signaling cascade between VEGFR-3 autophosphorylation and cell growth.

In a preferred embodiment, the method is practiced with a cell that expresses the mutant mammalian VEGFR-3 polypeptide and a wildtype mammalian VEGFR-3 polypeptide. Such cells are thought to better mimic the conditions in heterozygous individuals suffering from a VEGFR-3-mediated lymphatic disorder. In a highly preferred embodiment, the mutant and wildtype VEGFR-3 polypeptides are human. In the preferred embodiments, the mutant VEGFR-3 polypeptide comprises a leucine amino acid at the position corresponding to position 1114 of SEQ ID NO: 2; an arginine at the position corresponding to position 857 of SEQ ID NO: 2; a proline amino acid at the position corresponding to position 1041 of SEQ ID NO: 2; a proline amino acid at the position corresponding to position 1044 of SEQ ID NO: 2; or an asparagine at the position corresponding to position 1049 of SEQ ID NO: 2.

Additional features and variations of the invention will be apparent to those skilled in the art from the entirety of this application, including the drawing and detailed description, and all such features are intended as aspects of the invention.



Likewise, features of the invention described herein can be re-combined into additional embodiments that are also intended as aspects of the invention, irrespective of whether the combination of features is specifically mentioned above as an aspect or embodiment of the invention. Also, only such limitations which are described herein as critical to the invention should be viewed as such; variations of the invention lacking limitations which have not been described herein as critical are intended as aspects of the invention.

In addition to the foregoing, the invention includes, as an additional aspect, all embodiments of the invention narrower in scope in any way than the variations specifically mentioned above. Although the applicant(s) invented the full scope of the claims appended hereto, the claims appended hereto are not intended to encompass within their scope the prior art work of others. Therefore, in the event that statutory prior art within the scope of a claim is brought to the attention of the applicants by a Patent Office or other entity or individual, the applicant(s) reserve the right to exercise amendment rights under applicable patent laws to redefine the subject matter of such a claim to specifically exclude such statutory prior art or obvious variations of statutory prior art from the scope of such a claim. Variations of the invention defined by such amended claims also are intended as aspects of the invention.

#### **BRIEF DESCRIPTION OF THE DRAWINGS**

Figures 1A-1F depict pedigrees of six hereditary lymphedema families (Families 101, 106, 111, 135, 105, and 127, respectively) informative for linkage. Filled symbols represent individuals with clinically documented lymphedema. Crossed symbols represent individuals with an ambiguous phenotype. An ambiguous phenotype is defined as self-reported swelling of the limbs with no known cause, without a clinical diagnosis of lymphedema. Individuals of ambiguous phenotype were coded as disease status unknown for the linkage analysis. The proband in each family is indicated by an arrow.

Figure 2 is a graph summarizing VITESSE analysis of lymphedema families with markers localized to chromosome 5q34-q35. In the graph, filled circles represent analyses for Families 101, 105, 106, and 111; open boxes represent analyses for Families 101, 106, and 111; open circles represent the VEGFR-3 gene; and open triangles represent Family 135. The one LOD confidence interval lies completely

within the interval flanked by markers D5S1353 and D5S408 and overlaps the most likely location of *Flt4* (*VEGFR-3*). Linkage is excluded for the entire region for family 135.

5 Figure 3A-3B depict an alignment of portions of the human (top line, SEQ ID NO: 2) and murine (bottom line, GenBank Acc. No. P35917, SEQ ID NO: 19) VEGFR-3 amino acid sequences to demonstrate similarity. Identical residues are marked with a line, and highly conserved and less conserved differences are marked with two dots or a single dot, respectively. The location of various mutations that have been observed to correlate with a heritable lymphedema phenotype are indicated  
10 immediately beneath the aligned sequences.

### DETAILED DESCRIPTION OF THE INVENTION

Certain therapeutic aspects of the present invention involve the administration of Vascular Endothelial Growth Factor C or D polynucleotides and  
15 polypeptides. The growth factor VEGF-C, as well as native human, non-human mammalian, and avian polynucleotide sequences encoding VEGF-C, and VEGF-C variants and analogs, have been described in detail in International Patent Application Number PCT/US98/01973, filed 02 February 1998 and published on 06 August 1998 as International Publication Number WO 98/33917; in Joukov *et al.*, *J. Biol. Chem.*,  
20 273(12): 6599-6602 (1998); and in Joukov *et al.*, *EMBO J.*, 16(13): 3898-3911 (1997), all of which are incorporated herein by reference in the entirety. As explained therein in detail, human VEGF-C is initially produced in human cells as a prepro-VEGF-C polypeptide of 419 amino acids. A cDNA and deduced amino acid sequence for human prepro-VEGF-C are set forth in SEQ ID NOs: 3 and 4, respectively, and a  
25 cDNA encoding human VEGF-C has been deposited with the American Type Culture Collection (ATCC), 10801 University Blvd., Manassas, VA 20110-2209 (USA), pursuant to the provisions of the Budapest Treaty (Deposit date of 24 July 1995 and ATCC Accession Number 97231). VEGF-C sequences from other species have also been reported. See Genbank Accession Nos. MMU73620 (*Mus musculus*); and  
30 CCY15837 (*Coturnix coturnix*) for example, incorporated herein by reference.

The prepro-VEGF-C polypeptide is processed in multiple stages to produce a mature and most active VEGF-C polypeptide of about 21-23 kD (as

assessed by SDS-PAGE under reducing conditions). Such processing includes cleavage of a signal peptide (SEQ ID NO: 4, residues 1-31); cleavage of a carboxyl-terminal peptide (corresponding approximately to amino acids 228-419 of SEQ ID NO: 4 and having a pattern of spaced cysteine residues reminiscent of a Balbiani ring protein (BR3P) sequence [Dignam *et al.*, *Gene*, 88:133-40 (1990); Paulsson *et al.*, *J. Mol. Biol.*, 211:331-49 (1990)]) to produce a partially-processed form of about 29 kD; and cleavage (apparently extracellularly) of an amino-terminal peptide (corresponding approximately to amino acids 32-103 of SEQ ID NO: 4) to produce a fully-processed mature form of about 21-23 kD. Experimental evidence demonstrates that partially-processed forms of VEGF-C (*e.g.*, the 29 kD form) are able to bind the VEGFR-3 receptor, whereas high affinity binding to VEGFR-2 occurs only with the fully processed forms of VEGF-C.

Moreover, it has been demonstrated that amino acids 103-227 of SEQ ID NO: 4 are not all critical for maintaining VEGF-C functions. A polypeptide consisting of amino acids 113-213 (and lacking residues 103-112 and 214-227) of SEQ ID NO: 2 retains the ability to bind and stimulate VEGFR-3, and it is expected that a polypeptide spanning from about residue 131 to about residue 211 will retain VEGF-C biological activity. The cysteine residue at position 156 has been shown to be important for VEGFR-2 binding ability. However, VEGF-C  $\Delta C_{156}$  polypeptides (*i.e.*, analogs that lack this cysteine due to deletion or substitution) remain potent activators of VEGFR-3, and are therefore considered to be among the preferred candidates for treatment of lymphedema. (It has been shown that a VEGF-C C156S serine substitution analog promotes lymphatic growth when over-expressed in the skin of transgenic mice behind the K14 promoter, in a manner analogous to what was described in Jeltsch *et al.*, *Science*, 276:1423 (1997), incorporated herein by reference.) The cysteine at position 165 of SEQ ID NO: 4 is essential for binding to either receptor, whereas analogs lacking the cysteines at positions 83 or 137 compete with native VEGF-C for binding with both receptors and are able to stimulate both receptors.

An alignment of human VEGF-C with VEGF-C from other species (performed using any generally accepted alignment algorithm) suggests additional residues wherein modifications can be introduced (*e.g.*, insertions, substitutions, and/or deletions) without destroying VEGF-C biological activity. Any position at which

aligned VEGF-C polypeptides of two or more species have different amino acids, especially different amino acids with side chains of different chemical character, is a likely position susceptible to modification without concomitant elimination of function. An exemplary alignment of human, murine, and quail VEGF-C is set forth in Figure 5 of PCT/US98/01973.

Apart from the foregoing considerations, it will be understood that innumerable conservative amino acid substitutions can be performed to a wildtype VEGF-C sequence which are likely to result in a polypeptide that retains VEGF-C biological activities, especially if the number of such substitutions is small. By "conservative amino acid substitution" is meant substitution of an amino acid with an amino acid having a side chain of a similar chemical character. Similar amino acids for making conservative substitutions include those having an acidic side chain (glutamic acid, aspartic acid); a basic side chain (arginine, lysine, histidine); a polar amide side chain (glutamine, asparagine); a hydrophobic, aliphatic side chain (leucine, isoleucine, valine, alanine, glycine); an aromatic side chain (phenylalanine, tryptophan, tyrosine); a small side chain (glycine, alanine, serine, threonine, methionine); or an aliphatic hydroxyl side chain (serine, threonine). Addition or deletion of one or a few internal amino acids without destroying VEGF-C biological activities also is contemplated.

Without intending to be limited to a particular theory, the mechanism behind the efficacy of VEGF-C in treating or preventing lymphedema is believed to relate to the ability of VEGF-C to stimulate VEGFR-3 signaling. Administration of VEGF-C in quantities exceeding those usually found in interstitial fluids is expected to stimulate VEGFR-3 in human subjects who, by virtue of a dominant negative heterozygous mutation, have insufficient VEGFR-3 signaling.

The growth factor named Vascular Endothelial Growth Factor D (VEGF-D), as well as human sequences encoding VEGF-D, and VEGF-D variants and analogs, have been described in detail in International Patent Application Number PCT/US97/14696, filed 21 August 1997 and published on 26 February 1998 as International Publication Number WO 98/07832; and in Achen, *et al.*, *Proc. Nat'l Acad. Sci. U.S.A.*, 95(2): 548-553 (1998), both incorporated herein by reference in the entirety. As explained therein in detail, human VEGF-D is initially produced in human cells as a prepro-VEGF-D polypeptide of 354 amino acids. A cDNA and deduced amino acid sequence for human prepro-VEGF-D are set forth in SEQ ID Nos: 5 and 6,

respectively. VEGF-D sequences from other species also have been reported. See Genbank Accession Nos. D89628 (*Mus musculus*); and AF014827 (*Rattus norvegicus*), for example, incorporated herein by reference.

5 The prepro-VEGF-D polypeptide has a putative signal peptide of 21 amino acids and is apparently proteolytically processed in a manner analogous to the processing of prepro-VEGF-C. A "recombinantly matured" VEGF-D lacking residues 1-92 and 202-354 of SEQ ID NO: 6 retains the ability to activate receptors VEGFR-2 and VEGFR-3, and appears to associate as non-covalently linked dimers. Thus, preferred VEGF-D polynucleotides include those polynucleotides that comprise a  
10 nucleotide sequence encoding amino acids 93-201 of SEQ ID NO: 6.

The subject matter of the invention is further described and demonstrated with reference to the following examples.

### **EXAMPLE 1**

#### **Demonstration that hereditary lymphedema is linked to the VEGFR-3 locus**

15 The following experiments, conducted to identify a gene or genes contributing to susceptibility to develop lymphedema, demonstrated that hereditary lymphedema correlates, in at least some families, to the chromosomal locus for the VEGFR-3 gene.

### **OVERVIEW**

20 Families with inherited lymphedema were identified for the purpose of conducting a linkage and positional candidate gene analysis. Thirteen distinct families from the United States and Canada were identified through referrals from lymphedema treatment centers, lymphedema support groups, and from internet correspondence (worldwide web site at [www.pitt.edu/~genetics/lymph/](http://www.pitt.edu/~genetics/lymph/)). The study protocol was  
25 approved by the Institutional Review Board of the University of Pittsburgh and participants gave written informed consent. All members of the families were of western European ancestry. Forty members of one family ("Family 101") were examined during a family reunion by a physiatrist experienced in lymphedema treatment. Family members were considered affected with hereditary lymphedema if  
30 they exhibited asymmetry or obvious swelling of one or both legs. Members of the other 12 families were scored as affected if they had received a medical diagnosis of lymphedema, or if there were personal and family reports of extremity swelling or

asymmetry. Medical records were obtained to verify status whenever possible. For the purpose of linkage analysis, individuals with very mild or intermittent swelling, heavyset legs, obesity, or a history of leg infections as the only symptom were considered to have indeterminate disease status.

5 In the 13 families, 105 individuals were classified as affected, with a male:female ratio of 1:2.3. The age of onset of lymphedema symptoms ranged from prenatal (diagnosed by ultrasound) to age 55. When affected by normal matings were analyzed, 76 of 191 children were affected, yielding a penetrance of 80%. First degree relatives of affected individuals were considered at risk.

10 Biological samples were obtained from members of the thirteen families to conduct the genetic analyses. DNA was isolated from the EDTA-anticoagulated whole blood by the method of Miller *et al.*, *Nucleic Acids Res.*, 16: 1215 (1998), and from cytobrush specimens using the Puregene DNA isolation kit (Gentra Systems, Minneapolis, MN). Analysis of the markers used in the genome scan were performed  
15 by methods recognized in the art. [See Browman *et al.*, *Am. J. Hum. Genetic.*, 63:861-869 (1998); see also the NHLBI Mammalian Genotyping Service world-wide web sites ([www.marshmed.org/genetics/methods/pcr.htm](http://www.marshmed.org/genetics/methods/pcr.htm); and [www.marshmed.org/genetics/methods/gel.htm](http://www.marshmed.org/genetics/methods/gel.htm)).

Two-point linkage analysis was conducted using an autosomal  
20 dominant model predicting 80% penetrance in the heterozygous state, 99% penetrance in the homozygous state, and a 1% phenocopy rate. The frequency of the disease allele was set at 1/10,000. Microsatellite marker allele frequencies were calculated by counting founder alleles, with the addition of counts of non-transmitted alleles. Multipoint analysis was carried out using distances obtained from the Location  
25 Database (LDB-<http://cedar.genetics.soton.ac.uk/public.html>). Multipoint and 2-point analyses were facilitated using the VITESSE (v1.1) program. [O'Connell, J.R. and Weeks, D.E., (1995), *Nature Genet.*, 11:402-408].

## DETAILED DESCRIPTION OF METHODS AND RESULTS

30 The first family studied, Family 101, was a large, multi-generational family demonstrating early onset lymphedema. (See Fig. 1.) Forty individuals of this family were examined and DNA sampled. In addition, blood was obtained from another 11 members from mailing kits. Linkage simulation was performed using

SLINK [Weeks *et al.*, *Am. J. Hum. Genet.* 47:A204 (1990)] and linkage was analyzed using MSIM [Ott, J., *Proc. Nat. Acad. Sci. USA*, 86:4175-4178 (1989)] to estimate the potential power of two point linkage analysis in the family. Marker genotypes were simulated for a marker with heterozygosity of 0.875 under a linked ( $\theta=0$ ) and  
5     unlinked ( $\theta=0.5$ ) model using the 51 available individuals. The simulation showed that the power to detect linkage was greater than 90% for a LOD score threshold of  $Z(\theta)$  2.0. The false positive rate was less than 5%.

Shortly thereafter, two additional families (designated Families 106 and 111) segregating for autosomal dominant lymphedema were identified. These three  
10     families (Figures 1A-1C, Families 101, 106 and 111) were genotyped for 366 autosomal markers by the NHLBI Mammalian Genotyping Service (www.marshmed.org/genetics). Genotypes were checked for consistency using Pedcheck [O'Connell, J.R. and Weeks, D.E., *Am. J. Hum. Genet.*, 61:A288 (1997)]. Two point linkage analysis was performed using VITESSE [O'Connell, J.R. and  
15     Weeks, D.E., *Nature Genet.*, 11:402-408 (1995)]. The model for linkage assumed an autosomal dominant model of inheritance, a disease allele frequency of 0.0001 and a penetrance of 0.80.

The results from the genomic scan can be briefly summarized as follows. A summed LOD score of greater than 4.0 was observed from distal  
20     chromosome 5, markers *D5S1456*, *D5S817* and *D5S488*. The markers on distal chromosome 5q were the only markers having  $Z>3.0$ , the criteria established for statistical significance. LOD scores greater than 2.0 ( $\theta=0-0.15$ ) were also detected for chromosome 12 (*D12S391*  $Z=2.03$ , all families), and chromosome 21 (*D21S1440*  $Z=2.62$ , all families). The largest two-point LOD ( $Z=4.3$ ;  $\theta=0$ ) was observed for  
25     marker *D5S408*, localized to chromosome 5q34-q35.

This initial chromosomal mapping was further refined by genotyping the three affected families for eight additional markers localized to region 5q34-q35. Six of these were informative for linkage (*D5S653*, *D5S498*, *D5S408*, *D5S2006*, *D5S1353* and *D5S1354*). Linkage analysis of these markers using VITESSE yielded a 2-point  
30     LOD score of 6.1 at  $\theta=0$  for marker *D5S1354* (Table 1) and a maximum multipoint LOD score of 8.8 at marker *D5S1354* (Fig. 2). These findings supported the localization of a gene within chromosome band 5q34-q35 that is a predisposing factor in hereditary lymphedema.

**TABLE 1**

**LOD scores for individual families estimated over  
the interval defined by markers *D5S498* and *D5S2006*.**

		<b>Z(θ) 0.0</b>	<b>Z(θ) 0.01</b>	<b>Z(θ)0.05</b>	<b>Z(θ) 0.1</b>	<b>Z(θ) 0.2</b>
	<i>Locus D5S498</i>					
5	Family 101	-3.18	-2.33	-0.45	0.42	0.88
	Family 106	1.08	1.07	1.05	0.99	0.81
	Family 111	-0.85	-0.77	-0.53	-0.34	-0.13
	Family 105	1.22	1.20	1.11	0.98	0.72
	Family 135	-2.48	-1.85	-1.12	-0.75	-0.38
10	<i>Locus D5S1353</i>					
	Family 101	-2.99	-2.48	-1.21	-0.63	-0.18
	Family 106	0.28	0.29	0.35	0.38	0.38
	Family 111	-1.06	-1.02	-0.88	-0.72	-0.42
	Family 105	0.72	0.71	0.65	0.56	0.39
15	Family 135	-8.03	-4.18	-2.09	-1.13	-0.30
	<i>Locus D5S1354</i>					
	Family 101	6.09	6.02	5.69	5.21	4.07
	Family 106	1.42	1.40	1.32	1.20	0.96
	Family 111	0.21	0.22	0.23	0.24	0.22
20	Family 105	0.43	0.42	0.40	0.36	0.28
	Family 135	-6.88	-4.91	-3.20	-2.16	-1.07
	<i>Locus D5S408</i>					
	Family 101	2.80	2.74	2.50	2.20	1.56
	Family 106	0.66	0.68	0.73	0.76	0.71
25	Family 111	-1.70	-1.40	-0.80	-0.44	-0.10
	Family 105	0.42	0.41	0.38	0.35	0.27
	Family 135	-5.22	-4.24	-2.58	-1.67	-0.80



	<b>Z(θ) 0.0</b>	<b>Z(θ) 0.01</b>	<b>Z(θ)0.05</b>	<b>Z(θ) 0.1</b>	<b>Z(θ) 0.2</b>
<i>Locus D5S2006</i>					
Family 101	4.51	4.70	4.85	4.66	3.80
Family 106	1.17	1.16	1.11	1.03	0.83
Family 111	-1.32	-1.18	-0.82	-0.56	-0.25
Family 105	0.43	0.42	0.40	0.36	0.28
Family 135	-3.86	-3.20	-2.11	-1.45	-0.73

During the completion of the genome scan, an additional ten lymphedema families were ascertained. Two of these families (Families 105 and 135, see Figures 1E and 1D), were potentially informative for linkage and were genotyped for markers in the linked region. Examination of the two point LOD scores for the five informative families for markers in the linked region (Table 1) shows that four of the families (101, 105, 106 and 111) are consistent with linkage to chromosome 5q while family 135 excluded linkage across the entire region with LOD scores  $Z \leq -2.0$  for all markers. Multipoint linkage analysis of Families 101, 105, 106 and 111 (Fig. 2) yielded a peak LOD score of  $Z = 10$  at marker *D5S1354*. These findings support the existence of at least two loci which predispose to hereditary lymphedema.

The order of markers *D5S1353*, *D5S1354* and *D5S408* with respect to each other was uncertain. Multipoint linkage analysis using alternative orders for these markers gave similar results. Marker *D5S498* is a framework marker and marker *D5S408* is mapped 11.2 centimorgans distal to *D5S498*, based on the CHLC chromosome 5 sex averaged, recombination minimized map, version 3 (www.chlc.org). The physical distance between *D5S498* and *D5S408* is estimated as 1.45 megabases based on the Genetic Location Database (LDB) chromosome 5 summary map (cedar.genetics.soton.ac.uk/public\_html/).

Database analysis identified sixteen genes within this region. Two of these genes have been identified as having roles in development (*MSX2* and *VEGFR-3*). *MSX2* was considered an unlikely candidate gene for lymphedema because of its known involvement in craniofacial development [Jabs *et al.*, *Cell*, 75: 443-450 (1993)]. *VEGFR-3*, the gene encoding a receptor for VEGF-C, was selected as a better candidate gene for initial further study for the following reasons.

- (1) VEGFR-3 is expressed in developing lymphatic endothelium in the mouse [Kukk *et al.*, *Development*, 122: 3829-3837 (1996); and Kaipainen *et al.*, *Proc. Nat. Acad. Sci. USA*, 92: 3566-3570 (1995)];
- (2) expression of VEGFR-3 is induced in differentiating avian chorioallantoic membrane [Oh *et al.*, *Dev. Biol.*, 188:96-109 (1997)]; and
- (3) overexpression of VEGF-C, a ligand of VEGFR-3, leads to hyperplasia of the lymphatic vessels in transgenic mice [Jeltsch *et al.*, *Science*, 276: 1423-1425 (1997)].

To explore the potential role of VEGFR-3 in lymphedema, probands from the thirteen lymphedema families were screened for variation by direct sequencing of portions of the VEGFR-3 gene. The sequencing strategy used amplification primers generated based upon the *VEGFR-3* cDNA sequence (SEQ ID NO: 1) and information on the genomic organization of the related vascular endothelial growth factor receptor-2 (*VEGFR-2/KDR/flk-1*) [Yin *et al.*, *Mammalian Genome*, 9: 408-410 (1998)]. Variable positions (single nucleotide polymorphisms), the unique sequence primers used to amplify sequences flanking each variable site, and the method of detecting each variant are summarized in Table 2.

**TABLE 2**

**Location, amplification primer sequences, amplification conditions, and detection methods for five intragenic single nucleotide polymorphisms in the human VEGFR-3 gene**

Position in VEGFR-3 gene	Primer 1 sequence	Primer 2 sequence	Ann. temp.	[MgCl <sub>2</sub> ]	Base change	Detection Method
Exon 12, amino acid 641	tcaccatcgatccaagc (SEQ ID NO: 7)	agttctgcgtgagccgag (SEQ ID NO: 8)	56 °C	1.0 mM	C→T	Sequencing
Exon 24, amino acid 1114	caggacgggggtgactga (SEQ ID NO: 9)	gccacggcctgtctactg (SEQ ID NO: 10)	56 °C	1.0 mM	C→T	Sequencing
Exon 3, amino acid 175	ccagctcctacgtgttcg (SEQ ID NO: 11)	ggcaacagctggatgtca (SEQ ID NO: 12)	56 °C	1.0 mM	C→T	<i>HhaI</i>
65bp 3' to Exon 6	ctgtgagggcgtgggagt (SEQ ID NO: 13)	gtccttgagccactgga (SEQ ID NO: 14)	54 °C	1.5 mM	G→A	<i>StyI</i>
55bp 3' to Exon 2	cacacgtcatcgacccggtg (SEQ ID NO: 15)	ggcaacagctggatgtca (SEQ ID NO: 16)	56 °C	1.5 mM	C→T	<i>ApaI</i>

All amplifications were done for 35 cycles with denaturation at 94° for 30 seconds, annealing as above for 30 seconds, and extension at 72° for 30 seconds.

Amplification and sequencing primers were synthesized by the DNA Synthesis Facility, University of Pittsburgh. Amplification primers were tagged at the 5' end with the forward or reverse M13 universal sequence to facilitate direct sequencing. Amplimers were subjected to cycle sequencing using the dRhodamine terminator ready reaction kit or the Dye Primer ready reaction kit for -M13 and M13 Rev primers (Perkin Elmer) and analyzed on the Prism ABI 377 fluorescent sequencer. Sequences were aligned for further analysis using SEQUENCHER 3.0 (Gene Codes).

Genomic sequence from approximately 50% of the VEGFR-3 gene was determined in this manner, and five single nucleotide variants were observed. Two of the variants occurred in introns, and a third was a silent substitution in predicted exon 3. These intragenic polymorphisms were used to map the *VEGFR-3* gene. As shown in Figure 2, *VEGFR-3* maps within the region of chromosome 5q linked to the lymphedema phenotype, consistent with it being selected as a candidate gene. In two families, (Family 127, pedigree not shown, and Family 135), a C→T transition was identified at nucleotide position 1940 of the *VEGFR-3* cDNA (SEQ ID NO: 1). This nucleotide substitution is predicted to lead to a non-conservative substitution of serine (codon TCC) for proline (codon CCC) at residue 641 (putative exon 12, within the sixth immunoglobulin-like region of the receptor's extracellular domain) of the amino

acid sequence of the receptor (SEQ ID NO: 2). However, this sequence change was observed in 2 of 120 randomly selected individuals from the general population (240 alleles). Also, in one of the two families in which this variant was initially detected, family 135, linkage between lymphedema and chromosome 5q markers was excluded (Table 1 and Figure 2). In probands from the other ten families, wild type sequence was observed at nucleotide position 1940. Collectively, these results suggest that this P641S variant is not causative.

In one nuclear family (Family 127, pedigree shown in Figure 1F) a C-T transition was observed at nucleotide position 3360 (SEQ ID NO: 1) of the *VEGFR-3* cDNA. This nucleotide substitution is predicted to lead to a non-conservative substitution of leucine (codon CTG) for proline (codon CCG) at residue 1114 of the amino acid sequence of the receptor (SEQ ID NO: 2). This P1114L mutation is predicted to lie in the intracellular tyrosine kinase domain II involved in intracellular signaling [Pajusola *et al.*, *Cancer Res.*, 52:5738- 5743 (1992)]. Direct sequencing of predicted exon 24 of the *VEGFR-3* gene alleles from members of this family identified this substitution only in affected and at-risk family members. This sequence change was not observed in 120 randomly selected individuals of mixed European ancestry from the general population (240 alleles). In probands from the other 11 families, wild type sequence was observed at nucleotide position 3360.

Collectively, this data demonstrates that a missense mutation that causes a non-conservative substitution in a kinase domain of the VEGFR-3 protein correlates strongly with a heritable lymphedema in one family, and suggests that other mutations in the same gene may exist that correlate with heritable lymphedema in other families. As explained above, only a portion of the VEGFR-3 gene sequence was analyzed to identify this first mutant of interest. Additional sequencing, using standard techniques and using the known *VEGFR-3* gene sequence for guidance, is expected to identify additional mutations of interest that are observed in affected and at-risk members of other families studied.

**EXAMPLE 2**

**Demonstration that a C→T missense mutation at position 3360  
in the VEGFR-3 coding sequence results in a tyrosine kinase negative mutant**

The results set forth in Example 1 identified two missense mutations in  
5 the *VEGFR-3* coding sequence, one of which (C→T at position 3360) appeared to  
correlate with heritable lymphedema and one of which (C→T transition at position  
1940) did not. The following experiments were conducted to determine the  
biochemical significance of these mutations on VEGFR-3 biological activity.

To analyze how the two single amino acid substitutions affect the  
10 VEGFR-3-mediated signaling, the corresponding mutant receptor expression vectors  
were generated using site-directed mutagenesis procedures and expressed in 293T cells  
by transient transfection. The long form of human VEGFR-3 cDNA (SEQ ID NO: 1)  
was cloned as a *Hind* III-*Bam* HI fragment from the LTR-FLT4l plasmid [Pajusola *et*  
*al.*, *Oncogene* 8: 2931-2937 (1993)] into pcDNA3.1/Z(+) (Invitrogen). The P641S  
15 and P1114L mutants of VEGFR-3 were generated from this construct with the  
GeneEditor™ *in vitro* Site-Directed Mutagenesis System (Promega) using the  
following oligonucleotides (the C→T mutations are indicated with bold letters):

5'-CCTGAGTATCT**T**CCCGCGTCGC-3' (SEQ ID NO: 17) for P641S  
mutation; and  
20 5'-GGTGCCTCCCT**T**GTACCCTGGG-3' (SEQ ID NO: 18) for P1114L  
mutation.

For the transient expression studies, 293T cells were grown in  
Dulbecco's modified Eagle's medium (DMEM) supplemented with 10% fetal calf  
serum (GIBCO BRL, Life Technologies, Gaithersburg, MD), glutamine, and  
25 antibiotics. Cells were transfected with 20 µg of plasmid encoding the wild type or  
mutant VEGFR-3 forms using the calcium phosphate method, and harvested 36 hours  
after transfection for immunoprecipitation and Western blotting. Under these  
conditions, RTK overexpression results in ligand-independent activation, thus allowing  
the receptor phosphorylation to be studied. An empty vector was used for mock  
30 (control) transfections. (It will be appreciated that ligand stimulation assays of  
VEGFR-3 forms also can be employed, *e.g.*, as described in U.S. Patent No.  
5,776,755, incorporated herein by reference, using VEGF-C or VEGF-D ligands.)

In order to investigate the effect of the two VEGFR-3 mutants on the tyrosine phosphorylation of the VEGFR-3, Western blotting analysis was performed using anti-phosphotyrosine antibodies. The cell monolayers were washed three times with cold phosphate-buffered saline (PBS, containing 2 mM vanadate and 2 mM PMSF) and scraped into RIPA buffer (150 mM NaCl, 1 % Nonidet P40, 0.5 % deoxycholic acid sodium salt, 0.1 % SDS, 50 mM Tris-HCl, pH 8.0) containing 2 mM Vanadate, 2 mM PMSF, and 0.07 U/ml Aprotinin.

The cell lysates were sonicated and centrifuged for 10 minutes at 19,000 X g, and the supernatants were incubated for 2 hours on ice with 2 µg/ml of monoclonal anti-VEGFR-3 antibodies (9D9f9) [Jussila *et al.*, *Cancer Res.*, 58: 1599-604 (1998)]. Thereafter, Protein A sepharose (Pharmacia) beads were added and incubation was continued for 45 minutes with rotation at +4°C. The sepharose beads were then washed three times with ice-cold RIPA buffer and twice with PBS (both containing 2 mM vanadate, 2 mM PMSF), analyzed by 7.5 % SDS-PAGE and transferred to a nitrocellulose filter (Protran Nitrocellulose, Schleicher & Schuell, No. 401196) using semi-dry transfer apparatus. After blocking the filter with 5 % BSA in TBS-T buffer (10 mM Tris, pH 7.5, 150 mM NaCl, 0.05 % Tween 20), the filters were incubated with the phosphotyrosine-specific primary antibodies (Upstate Biotechnology, #05-321), followed by biotinylated goat-anti-mouse immunoglobulins (Dako, E0433) and Biotin-Streptavidin HRP complex (Amersham, RPN1051). The bands were visualized by the enhanced chemiluminescence (ECL) method.

After analysis for phosphotyrosine-containing proteins, the filters were stripped by washing for 30 minutes at +50°C in 100 mM 2-mercaptoethanol, 2 % SDS, 62.5 mM Tris-HCl, pH 6.7, with occasional agitation. The filters were washed with TBS-T, blocked again with BSA as described above, and analyzed for the presence of VEGFR-3 using the 9D9f9 antibodies and HRP-conjugated rabbit-anti-mouse immunoglobulins (Dako, P0161).

The Western analyses revealed that the P641S mutant receptor was phosphorylated normally, *i.e.*, in a manner similar to the wild type control. However, the proteolytic processing of the P641S receptor protein may be affected, as the 175 kD and 125 kD polypeptides seemed to have a higher relative density when compared to the 195 kD form.

In contrast, no phosphorylated P1114L mutant protein was detected using the phosphotyrosine antibodies. The expression of similar amounts of the VEGFR-3 protein (normal and both mutants) was confirmed using the monoclonal 9D9f9 antibody, which is directed towards the extracellular domain of the VEGFR-3. Both the P641S and the P1114L mutant VEGFR-3 migrated slightly faster than the wild type VEGFR-3 in the gel electrophoresis.

In order to analyze the possible dominant negative effect of the P1114L mutant on the wild-type receptor, a second, similar set of experiments were performed wherein the 293T cells were transfected with an increasing amount of the P1114L expression vector in combination with decreasing amounts of the wild type vector. Wild type to mutant ratios of 1:0, 3:1, 1:1, 1:3 and 0:1 were used. The cells were lysed 48 hours after transfection and the lysates were analyzed by immunoprecipitation and Western blotting as described above. These experiments permitted evaluation of whether the mutant protein interferes with wild type protein phosphorylation and estimation of the minimal amount of the WT protein needed for observable tyrosyl autophosphorylation. Immunoprecipitates from cells transfected with only the WT plasmid revealed WT protein that was strongly phosphorylated in this experiment (lane 2), whereas immunoprecipitates from cells transfected with only the mutant plasmid were again inactive (unphosphorylated).

Interestingly, when transfection was made using 75% of WT and 25 % of mutant plasmid, the phosphorylation of the receptors was decreased by about 90%. This result strongly suggests that the P1114L mutant receptor forms heterodimers with the WT receptor, but cannot phosphorylate the WT receptor, thus failing to activate it. Under this theory, the WT receptor monomers in the heterodimers would also remain inactive, causing a disproportionate decrease of the total amount of activated receptor, when co-transfected with the mutant. Wildtype-wildtype homodimers would remain active and be responsible for the observed signaling. When the wild type and mutant receptor expression vectors were transfected at a 1:1 ratio, the VEGFR-3 phosphorylation was about 4% of the wild type alone, whereas at a 1:3 ratio, no tyrosine phosphorylation of VEGFR-3 was observed.

The foregoing results are consistent with the linkage analyses in Example 1: the mutation at position 641 that did not appear to correlate with lymphedema also did not appear to be dysfunctional, whereas the mutation at position

1114 appeared to cause a dominant negative mutation that shows no tyrosine phosphorylation alone and that drastically reduces VEGFR-3 signaling in cells expressing both the mutant and wild type VEGFR-3 genes.

Collectively, these data indicate that the P1114L VEGFR-3 mutant is  
5 unable to act as a part of the signaling cascade, and also acts in a dominant negative manner, thus possibly interfering partially with the activation of the wild type VEGFR-3. Such effects of the mutation may eventually lead to lymphedema.

### **EXAMPLE 3**

#### **Treatment of lymphedema with a VEGFR-3 ligand**

10 The data from Examples 1 and 2 collectively indicate a causative role in heritable lymphedema for a mutation in the *VEGFR-3* gene that interferes with VEGFR-3 signaling. Such a mutation behaves in an autosomal dominant pattern, due to the apparent necessity for receptor dimerization in the signaling process. However, the data from Example 2 suggests that some residual signaling may still occur in  
15 heterozygous affected individuals, presumably through pairing of VEGFR-3 proteins expressed from the wild type allele. The following experiments are designed to demonstrate the efficacy of VEGFR-3 ligand treatment in such affected individuals, to raise VEGFR-3 signaling to levels approaching normal and thereby ameliorate/palliate the symptoms of hereditary lymphedema.

20 Initially, an appropriate animal model is selected. Several potential animal models have been described in the literature. [See, e.g., Lyon *et al.*, *Mouse News Lett.* 71: 26 (1984), *Mouse News Lett.* 74: 96 (1986), and *Genetic variants and strains of the laboratory mouse*, 2nd ed., New York: Oxford University Press (1989), p. 70 (*Chylous ascites* mouse); Dumont *et al.*, *Science*, 282: 946-949 (1998)  
25 (heterozygous VEGFR-3 knockout mouse); Patterson *et al.*, "Hereditary Lymphedema," *Comparative Pathology Bulletin*, 3: 2 (1971) (canine hereditary lymphedema model); van der Putte, "Congenital Hereditary Lymphedema in the Pig," *Lympho*, 11: 1-9 (1978); and Campbell-Beggs *et al.*, "Chyloabdomen in a neonatal foal," *Veterinary Record*, 137: 96-98 (1995).] Those models which are determined to  
30 have analogous mutations to the VEGFR-3 gene are preferred. Analogous mutations would include mutations affecting corresponding residues and also mutations affecting different residues but causing similar functional alterations. The *Chylous ascites*



mouse VEGFR-3 gene contains a missense mutation at a position corresponding to residue 1053 of SEQ ID No. 2, which maps to the catalytic pocket region of the tyrosine kinase catalytic domain. Thus, the "*Chy*" mouse is expected to display similar functional alterations to human mutations affecting tyrosine kinase activity, a prediction which can be confirmed by functional assays such as those described in Example 2. In a preferred embodiment, "knock in" homologous recombination genetic engineering strategies are used to create an animal model (*e.g.*, a mouse model) having a VEGFR-3 allelic variation analogous to the human variations described herein. [See, *e.g.*, Partanen *et al.*, *Genes & Development*, 12: 2332-2344 (1998) (gene targeting to introduce mutations into another receptor protein (FGFR-1) in mice).] For example, the P1114L mutation in human VEGFR-3 occurs in a VEGFR-3 region having highly conserved amino acid identity with murine VEGFR-3 (Genbank Accession No. L07296). Thus, a corresponding P1114L can be introduced into the murine VEGFR-3 by "knock-in" homologous recombination. Optionally, such mice can be bred to the heterozygous VEGFR-3 knockout mice or *Chy* mice described above to further modify the phenotypic severity of the lymphedema disease.

The mice as described above are treated with a candidate therapeutic, *e.g.*, a recombinant mature form of VEGF-C, at various dosing schedules, *e.g.*, once daily by intravenous (IV) or intramuscular (IM) injection at a dose of 1-1000 ng/g body weight, preferably 10-100 ng/g, which should result in a peak level saturating VEGFR-3 ( $K_d$  about 150 pM) but not VEGFR-2 ( $K_d$  around 400 pM). For VEGFR-3-specific forms, such as VEGF-C $\Delta$ C<sub>156</sub>, even higher dosing is contemplated, to sustain VEGFR-3-saturating physiological concentrations for longer periods. Direct IM injection at multiple sites in the muscles of affected extremities is a preferred route of administration. The dosing is adjusted according to the efficacy of the treatment and the presence of possible side effects due to the lowering of blood pressure, which has been observed in response to VEGF administration IV. The efficacy of treatment is measured via NMRI imaging of the water content and volume of swelling of the abdomen and the extremities of the animals. The amount of fluid in the abdominal cavity is estimated and the animals are weighed during the follow-up.

In studies using VEGFR-3  $-/+$  x *Chy* mice progeny, the animals will also have the  $\beta$ -galactosidase marker in their lymphatic endothelium. After a successful treatment, the treated and non-treated experimental animals and VEGFR-3

-/+ controls are killed and their lymphatic vessels are visualized by  $\beta$ -gal and antibody staining. The staining patterns of experimental and control animals are compared for vessel diameter, numbers of endothelial cells, density of blood and lymphatic vessels, and nuclear density/section surface area for the estimation of tissue oedema.

5 Such experiments are repeated with various candidate therapeutics (e.g., VEGF-C or VEGF-D recombinant polypeptides; VEGF-C and VEGF-D gene therapy vectors; and combinations thereof) at various dosing schedules to determine an optimum treatment regimen.

#### **EXAMPLE 4**

##### **Chromosomal structure of the human *VEGFR-3* gene**

10 Sequencing and mapping of human DNA corresponding to the *VEGFR-3* locus has indicated that this gene consists of thirty exons separated by twenty-nine introns of varying size. The exon intron organization is summarized as follows:

	<b><u>EXON NUMBER</u></b>	<b><u>Bp of SEQ ID NO: 1 size (bp)</u></b>	<b><u>INTRON SIZE</u></b>
15	1	20-77 58 bp	unknown
	2	78-174 97 bp	>1kb
20	3	175-419 245 bp	218 bp
	4	420-532 113 bp	120 bp
25	5	533-695 163 bp	107 bp
	6	696-835 140 bp	269 bp
	7	836-1004 169 bp	261 bp
30	8	1005-1122 118 bp	>1 kb
	9	1123-1277	

Accession	Gene	Gene length (bp)	Gene size (kb)
5	10	1278-1440 163 bp	>1 kb
	11	1441-1567 127 bp	unknown
	12	1568-1676 109 bp	unknown
	13	1677-2039 363 bp	293 bp
	14	2040-2186 147 bp	99 bp
10	15	2187-2318 132 bp	approx. 160 bp
15	16	2319-2425 107 bp	301 bp
	17	2426-2561 139 bp	>464 bp
	18	2562-2666 105 bp	unknown
20	19	2667-2780 114 bp	143 bp
25	20	2781-2869 89 bp	>1 kb
	21	2870-3020 151 bp	unknown
	22	3021-3115 95 bp	unknown
	23	3116-3238 123 bp	unknown
30	24	3239-3350 112 bp	974 bp
	25	3351-3450 100 bp	400 bp

	26	3451-3557 107 bp	unknown
	27	3558-3705 148 bp	>1 kb
5	28	3706-3826 121 bp	unknown
	29	3827-3912 86 bp	unknown
10	30a (Flt4 short)	3913-4111 199 bp	3.7 kb
	30b (Flt4long)	3913-4416 >504 bp	(CDS 504 bp)

The foregoing information permits rapid design of oligonucleotides for amplifying select portions of the VEGFR-3 gene from genomic DNA, or RNA, or cDNA, to facilitate rapid analysis of an individual's *VEGFR-3* coding sequence, to determine whether the individual possesses a mutation that correlates with a lymphedema phenotype.

### **EXAMPLE 5**

#### **Identification of additional non-conservative missense mutants**

Using procedures essentially as described in Example 1, the VEGFR-3 coding sequences from additional affected and unaffected individuals from families having members suffering from heritable lymphedema were studied. The analysis focused on families with statistical linkage to chromosome 5q as described in Example 1. The additional analysis included the PCR amplification and sequencing of Exon 17, Exon 22, and Exon 23 sequences with the following PCR primers:

	Exon 17-1	5'-CATCAAGACGGGCTACCT-3' (SEQ ID NO: 23)
	Exon 17-2	5'-CCGCTGACCCACACCTT-3' (SEQ ID NO: 24)
	Exon 22-1	5'-GAGTTGACCTCCCAAGGT-3' (SEQ ID NO: 25)
	Exon 22-2	5'-TCTCCTGGACAGGCAGTC-3' (SEQ ID NO: 26)
30	Exon 23-1	5'-GAGTTGACCTCCCAAGGT-3' (SEQ ID NO: 27)
	Exon 23-2	5'-TCTCCTGGACAGGCAGTC-3' (SEQ ID NO: 28)

These additional studies identified four additional non-conservative missense mutations in evolutionarily conserved amino acids in kinase domains I and II of human VEGFR-3. Each mutation, shown in Table 3 below, was observed in a single independently ascertained family, and in each family, the mutation co-segregates with individuals suffering from, or considered at risk for developing, lymphedema. None of these mutations were observed in the *VEGFR-3* genes in a random sample of more than 300 chromosomes from individuals from families unaffected with heritable lymphedema.

**TABLE 3**  
Mutations in VEGFR-3 causing Hereditary Lymphedema\*

Exon	Nucleotide Substitution**	Amino Acid Substitution	Functional Domain
24	C3360T	P1114L	Kinase 2
17	G2588A	G857R	Kinase 1
23	G3141C	R1041P	Kinase 2
23	T3150C	L1044P	Kinase 2
23	G3164A	D1049N	Kinase 2

\* Numbers indicate nucleotide or amino acid positions in SEQ ID NOs: 1 and 2.

\*\*It will be appreciated that, since DNA is double-stranded, each mutation could be characterized in two equivalent ways, depending on whether reference is being made to the coding or the non-coding strand.

Referring to SEQ ID NO: 2, the kinase domains of VEGFR-3 comprise approximately residues 843-943 and residues 1009-1165. Within these domains, molecular modeling suggests that residues G852, G854, G857, K879, E896, H1035, D1037, N1042, D1055, F1056, G1057, E1084, D1096 and R1159 are of particular importance in comprising or shaping the catalytic pocket within the kinase domains. See van Der Geer and Hunter, *Ann. Rev. Cell. Biol.*, 10: 251-337 (1994); and Mohammadi *et al.*, *Cell* 86: 577-587 (1996). Thus, this data identifying additional mutations implicate missense mutations within a kinase domain of the VEGFR-3 protein as correlating strongly with a risk for developing a heritable lymphedema phenotype. Mutations which affect residues in and around the catalytic pocket appear particularly likely to correlate with lymphedema. The P1114L mutation, though not

situated within the catalytic pocket, is postulated to cause a conformational alteration that affects the catalytic pocket. The G857R mutation is postulated to block the catalytic pocket and/or the ATP binding site of the kinase domain.

### **EXAMPLE 6**

#### **5                    Functional Analysis of Additional *VEGFR-3* missense mutations**

Using procedures essentially as described above in Example 2, the functional state of the G857R, L1044P, and D1049N mutations were analyzed. (PLCLB buffer, comprising 150 mm NaCl, 5% glycerol, 1% Triton X-100, 1.5M MgCl<sub>2</sub>, 50 mm HEPES, pH 7.5, was substituted for RIPA buffer described in Example 2 for immunoprecipitation and Western blotting protocols.) A *VEGFR-3*-encoding construct comprising the G857R mutation was generated from the long form of human *VEGFR-3* cDNA using the oligonucleotide:

5'-CGG CGC CTT CAG GAA GGT GGT-3' (SEQ ID NO: 20)

A construct comprising the L1044P mutation was generated from the long form of human *VEGFR-3* cDNA using the oligonucleotide:

5'-CGG AAC ATT CCG CTG TCG GAA-3' (SEQ ID NO: 21)

A construct comprising the D1049N mutation was generated from the long form of human *VEGFR-3* cDNA using the oligonucleotide:

5'-GTC GGA AAG CAA CGT GGT GAA-3' (SEQ ID NO: 22).

20                    The constructs were transiently transfected into 293T cells and harvested for Western blotting essentially as described in Example 2, except for the buffer substitution described above. In contrast to wild type *VEGFR-3* and *VEGFR-3* containing the P641S mutation, no phosphorylated G857R or L1044P mutant protein was detected using the phosphotyrosine antibodies, consistent with the results that had been observed for P1114L. The expression of similar amounts of the *VEGFR-3* protein was confirmed using the monoclonal 9D9f9 antibody, which is directed towards the extracellular domain of the *VEGFR-3* in the Western blotting. This data suggested that these observed mutations did indeed affect *VEGFR-3* kinase function. The D1049N mutant appeared to retain at least some tyrosine kinase activity. It is also noteworthy that *VEGFR-1* and *VEGFR-2* contain an asparagine residue at the position in their tyrosine kinase domains which corresponds to position 1049 of *VEGFR-3*.

Together, these data suggest that the D1049N variation may only be an allelic variant that correlates with hereditary lymphedema, rather than a causative mutation.

To determine whether the VEGFR-3 mutants function in a dominant negative manner, each construct was co-transfected at varying ratios with wild type receptor into 293T cells essentially as described in Example 2. Unlike the results  
5 observed for P1114L and described in Example 2, neither the G857R mutant nor the L1044P mutant seemed to interfere with phosphorylation of the co-transfected wild type receptor.

The absence of a dominant negative effect in these experiments does  
10 not foreclose a conclusion that the mutations described above are causative. It has been found that a significant fraction of ligand-activated receptor tyrosine kinases traffic to the lysosomal compartment after internalization, where they are degraded. However, receptors which are not ligand-activated preferentially recycle back to the cell surface after internalization. Thus, it is possible that the turnover time of the  
15 weakly phosphorylated mutant receptor is significantly longer than that of the wild type receptor protein. If this were true, the amount of the mutant receptor on the endothelial cell surface could be considerably higher than the amount of the phosphorylated and rapidly internalized wild type receptor, and any available ligand would thus bind a disproportionately high number of mutant receptors. Both a possible  
20 dominant negative effect of the mutant receptor and an abnormally long half-life of the tyrosine kinase negative mutant receptor could eventually lead to lymphedema. Alternatively, a mutation that merely decreases (but does not eliminate) VEGFR-3 tyrosine kinase activity may display a constitutive low level of internalization and degradation that is insufficient to trigger sufficient downstream signalling, but  
25 decreases the effective concentration of VEGFR-3 on cell surfaces for ligand binding and effective activation, leading eventually to lymphedema.

While the present invention has been described in terms of specific embodiments, it is understood that variations and modifications will occur to those in the art, all of which are intended as aspects of the present invention. Accordingly, only  
30 such limitations as appear in the claims should be placed on the invention.